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Title:
Perfect score:
Total number of hits satisfying chosen parameters:
                                                   Searched:
                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                               Scoring table:
                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                     US-09-331-631A-5_COPY_76_144
381
                                                                                                                                                                                                                                               March 1, 2001, 15:52:37; Search time 170.72 Seconds (without alignments) 27.443 Million cell updates/sec
                                                195891 segs, 67900655 residues
                                                                                                                                                              1 NRQRDPQQQYEQCQKRCQRR.....EEQQREDEEKYEERMKEGDN 69
                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

195891

RESULT S22477

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	NO.	Result
92.5	93	93	93	93	93.5	94	94	94	95	95	95.5	(13	97.5	97.5	97.5	97.5	99	100	101	102	103	105.5	114.5	115	128	145.5	147.5	173	Score	
24.3	24.4	24.4	24.4	24.4	24.5	24.7	24.7				25.1	5	25.6	5	5	5	6	26.2	6.	6	7.	7.	0	0.	33.6	8	8	45.4	Match	
1403	849	523	429	139	781	1085	648	233	905	524	1023	483	1233	1027	877	839	1390	1407	1737	613	1898	385	1038	810	605	588	509	566	Lengin	
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	7	hypothetical prote	apolipoprotein A-I	ct		U	protein kinase (EC	hypothetical prote	regulatory protein	se-	glutactin - fruit	62K sucrose-bindin	serine/threonine p	hypothetical prote	II INCEN	NP			۵	pr				_			alpha-globulin typ	vicilin precursor	Description	

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
	88	88	88	88	88	88	88.5	89	89	89.5	90	90	91	91.5	91.5	91.5
	23.1	23.1	23.1	23.1	23.1	23.1	23.2	23.4	23.4	23.5	23.6	23.6	23.9	24.0	24.0	24.0
	779	777	768	766	447	292	407	582	285	758	1344	678	385	573	540	406
	Ν	2	N	N	2	N	N	N	1	N	N	N	N	N	N	ν
ALIGNMENTS	E54024	F54024	H54024	G54024	S52391	JE0233	T02258	B53234	146207	S54522	T42637	A54514	T20410	A53234	S21825	T24492
HS.	-		protein kinase (EC	protein kinase (EC	centrosomin B - mo	troponin-I - scall	globulin1 - maize	vicilin-like stora	involucrin - dog	hypothetical prote	hypothetical prote	glutamic acid-rich	hypothetical prote	globulin-1S, GLB1S	vicilin-like stora	hypothetical prote

ALIGNMENTS

RESULT 2 \$08059 slipha-globulin type B precursor (tandem 1) - upland cotton (fragment) N;Alternate names: seed storage protein C;Species: Gossypium hirsutum (upland cotton) C;Date: 31-Mar-1990 *sequence_revision 31-Mar-1990 *text_change 30-Sep-1993 C;Accession: \$08059 R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987 A;Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. A;Reference number: \$06398 A;Accession: \$08059 A;Status: not compared with conceptual translation	QRDPQQQYEQCOKRCORRETEPRHMQICQQRCERRYEKEKRKQQ	A;Cross-references: EMBL:X02026 C;Genetics: A;Introns: 211/1; 269/3; 296/3; 391/3; 502/1 C;Superfamily: 91ycinin C;Keywords: seed; storage protein F;1-24/Domain: signal sequence #status predicted <sig> F;25-566/Product: vicilin #status predicted <mat> Query Match Best Local Similarity 32.6%; Pred. No. 1.5e-07; Matches 31; Conservative 17; Mismatches 15; Indels 32: Gaps 1:</mat></sig>	R:MCHenry, L.; Fritz, P.J. Plant Mol. Biol. 18, 1173-1176, 1992 A;Title: Comparison of the structure and nucleotide sequence of vicilin genes of coco A;Reference number: \$22477; MUID:92288309 A;Reference number: \$22477; MUID:92288309 A;Recession: \$22477 A;Molecule type: DNA A;Residues: 1-566 <mch> A;Residues: 1-566 <mch> A;Cross-references: EMBL:X62625 A;Accross-references: EMBL:X62625 A;Accross-references: EMBL:X62625 A;Cross-references: EMBL:X62625 A;Cross-references: EMBL:X62625</mch></mch>	vicilin precursor - cacao C:Species: Theobroma cacao (cacao) C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999 C:Accession: S22477; S22478, S18105; S22050
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A; Residues: 1-81 <CH2> C; Comment: This is a seed storage protein. C; Comment: This is a seed storage protein. C; Superfamily: glycinin c; Keywords: glycoprotein; seed; storage protein C; Keywords: glycoprotein; seed; storage protein e; 1-25/Domain: signal sequence #status predicted <SIG> F; 16-588/Product: alpha-globulin storage proprotein #st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Gossypium hirsutum (upranu cocco., C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change C; Accession: A30838; S06911 R; Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L. R; Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure iii, L. Plant Mol. Biol. 7, 475-489, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-509 < CHL>
C; Superfamily: glycinin
                                         C; Accession: S06398 R; Chlan, C.A.; Borro
                                                                             N;Alternate names: seed storage protein C;Species: Gossyplum hirsutum (upland cotton) C;Date: 31-Mar-1990 #sequence_revision 31-Mar
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    A; Title: Developmental biochemistry
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A; Accession: S06911
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A; Residues: 1-588 < CHL>
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                         Biol.
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28; Conserv
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29; Conservative
                      Borroto, K.; Kamalay, J.A.;
l. 9, 533-546, 1987
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    cottonseed
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embryogenesis
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protein Pv100 [imported] - winter squash (C;Species: Cucurbita maxima (winter squash) C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change C;Accession: T44430 R; Kondo, M; Nishimura, M.; Hara-Nishim R;Yanada, K.; Shimada, T.; Kondo, M; Nishimura, M.; Hara-Nishim J. Biol. Chem. 274, 2563-2570, 1999 A;Title: Multiple functional proteins are produced by cleaving A;Reference number: Z22767; MUID:99107919
A; Genome:
A; Mobile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S06398
A; Accession: S06398
A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Meslidues: 1-605 < CHL>
C; Superfamily: glycinin
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-605/Product: alpha-globulin type A #status predic
                                      A;Gene: rep
                                                              C; Genetics:
                                                                             A; Experimental source:
                                                                               A;Cross-references: EMBL:AF000580; NID:g3068582; PIDN:AAC14390.1; PID:g3068583 A;Experimental source: strain WS2162
                                                                                                                                         A;Status: preliminary; translated A;Molecule type: DNA
                                                                                                                                                                                                       R;Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Pilkington, K.J.; Kiyosawa, H.; H Genetics 148, 1117-1125, 1998
A;Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to the Dd A;Reference number: Z14684; MUID:98198836
                                                                                                                                                                                                                                                                                                          C; Species: Dictyostelium discoideum C; Date: 24-Mar-1999 #sequence_revision
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A; Residues: 1-810 < YAM>
A; Cross-references: EMB
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e: plasmid
element:
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                                                                                                                                                                                                                                                                                                                                                   homolog - slime mold (Dictyostelium discoideum) plasmid Ddp5
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32.1%;
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                                                                                                                                                                 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.03
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M.; Nishimura, M.; Hara-Nishimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 128; DB 2; Pred. No. 0.00085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                 GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                              24-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                                                          #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cleaving Asn-Gln bonds of a sin
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                                                                                                                                                                                                                                                                                                            29-Oct-1999
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plasmid

Ddp5

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A;Molecule type: DNA
A;Residues: 1-1898 <-LEE>
A;Cross-references: GB:L09190; NID:g292835; PIDN:AAA65582.1; PID:g292836
A;Note: authors translated the codon AGG for residue 1714 as Pro
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root covalent modifications to this protein include conversion of arginine to citrulline an C;Genetics:
A;Gene: GDB:HH
A;Cross-references: GDB:136223; OMIM:190370
A;Map position: 1q21-1q21
C;Superfamily: trichohyalin; calmodulin repeat homology
C;Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trichohyalin - human (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: 03-May-1994 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999 (Spacession: A4597) (Species: 03-May-1994 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999 (Species: 03-May-1994 #sequence_revision 01-Mar-1996 #seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ed (cross-linking) protein.
A; Reference number: A45973; MUID:93280194
A; Accession: A45973
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A:Introns: 12/1; 106/3; 171/2; 335/2
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A;Accession: T19201
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-385 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C11G6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       996 QREQE 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 ERMKE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QREDEEKYEERMKE 66
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28.4%;
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A;Map position: 6, aldB-cabA2
C;Superfamily: myosin motor domain homology
F;62-874/Domain: myosin motor domain homology #status atypical <MMO>
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A;Residues: 1-1737 <GET>
A;Cross-references: GB:AF090533; NID:g5714395; PIDN:AAD47903.1; PID:g5714396
A;Experimental source: strain AX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Dictyostelium discoldeum
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000
C:Accession: A59235
C:Accession:
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                                                                                                                                                                                                                                                                                                                            A; Experimental C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to GenBank, September 1998 A; Description: Identification of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Thehes 18; Conserv
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C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
C;Accession: S27770
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                                                                                                                                                                                                                                                                                       A; Gene: myoM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; not compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A59235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Дb
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A; Residues: 1-613 <BES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unconventional myosin heavy chain MyoM - slime mold (Dictyostelium discoideum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;49-81/Domain: calmodulin repeat homology <EF2>
   Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ERMKEGDN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 DEEKYEERMKE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RORDPOQQYEQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQREDEEKYE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RQRDPQQQYEQCQK-----RCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQRE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQRELQEEEEQLRKLERQELRRERQEEEQQQQRLRREQQLRRKQEEERREQQEERREQQE 326
                                        Similarity
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       Conservative
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35.8%;
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31.0%;
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                                    Score 101;
Pred. No. 0.
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Pred. No. 0.12;
7; Mismatches
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Pred. No. 0.25;
       Mismatches
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                             DB
.34;
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                                                                     2;
       19;
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                                                                     Length 1737;
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       Indels
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1 NRQRDPQQQYEQCQKRCQRRETEPRHMQICQQRCERRYEKE~KRKQQKRYEEQQREDEEK 59

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R;Fietz, M.J.; Rogers, G.E. submitted to the EMBL Data Library, December 1992 A:Description: Examination of the gene encoding rabbit
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J. Biol. Chem. 273, 24654-24659, 1998
A;Title: Dictyostelium TRFA homologous to yeast
A;Reference number: Z17852; MUID:98406112
A;Accession: T14004
                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T14004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: trichohyalin; calmodulin repeat homology C;Keywords: calcium binding; citrulline; EF hand; hair; F;49-81/Domain: calmodulin repeat homology <EF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Oryctolagus
C; Date: 12-Mar-1993 #se
C; Accession: S28589
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A; Residues: 1-1390 <:
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T14004
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A;Residues; 1-1407 <FIE>
A;Cross-references: EMBL:Z19092; NID:g1746; PIDN:CAA79519.1; PID:g1747
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root sl
Covalent modifications to this protein include conversion of arginine to citrulline and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                     A; Introns: 333/3;
                                                                                                                                                                                                                   A; Gene:
                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                               Query Match
Best Local
                                                                                                              Matches
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Best Local
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                                                                                                                           Local Similarity
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                                                                  2 RORDPOQOYEQCOKRCORRETEPRHMOICOORCERRYEKEKRKOOKRYEEQOREDEEKYE 61
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   ERMKEGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRDPQQQYEQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQK-------RYEEQQR 54
                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     slime mold (Dictyostelium discoideum)
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                     364/3; 637/1
                                                                                                                                                                                                                                                      <SAI>: EMBL: AB009080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gus cuniculus (domestic rabbit)
#sequence_revision 01-Mar-1996
                                                                                                                           26.0%;
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                                                                                                                         Score
Pred.
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                                                                                                                                                                                                                                                      NID:d1228566; PID:d1034109; PIDN:BAA33143.1
                                                                                                            Mismatches
                                                                                                                       99; DB 2;
No. 0.42;
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.35;
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                                                                                                                                             Length 1390;
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                                                                                                          Indels
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                                                                                                         Gaps
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                                                                                      RESULT
T46481
                hypothetical protein DKFZp434A025.1 - h C;Species: Homo sapiens (man) C;Date: 04-Feb-2000 #sequence_revision C;Accession: T46481
   R; Duesterhoeft,
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A; Residues: 1-877 < MAC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A48482; MUID:94012983 A;Accession: I50591
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A;Title: Molecular analysis of the INCENPs (inner centromere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
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C; Species: Gallus gallus (chicken)
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A;Residues: 1-839 <MAC>
A;Cross-references: EMBL:Z25419; NID:g414108; PIDN:CAA80906.1;
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A;Accession: I50590
A;Status: preliminary; translated from GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Mackay, A.M.; Eckley, D.M.; Chue, C.; Earnshaw, W.C
J. Cell Biol. 123, 373-385, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         class I INCEMP protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
C;Accession: ISO590
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Matches 22
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                666 QERKKE
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nes 22; Conser
                                                                                                                                                                                                 61 EERMKE 66
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Lauber,
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                                                                      human (fragment)
                                 04-Feb-2000 #text_change 04-Feb-2000
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Η. W.
Gassenhuber, J.;
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submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23035
A:Accession: T46481
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1027 <AAA>
A:Coss: references: EMBL:AL137755
A:Cross-references: EMBL:AL13775
A:Cross-references: EMBL:AL13775
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